

## WEST Search History

DATE: Monday, October 17, 2005

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L1	lipase	20084
<input type="checkbox"/>	L2	L1 and senescence	324
<input type="checkbox"/>	L3	L2 and transgenic	188
<input type="checkbox"/>	L4	L3 and plant	164

END OF SEARCH HISTORY

Connecting via Winsock to STN

10/674,540

Welcome to STN International! Enter x:x

LOGINID:SSPTAVXK1638

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

\* \* \* \* \* Welcome to STN International \* \* \* \* \*

NEWS 1 Web Page URLs for STN Seminar Schedule - N. America  
NEWS 2 "Ask CAS" for self-help around the clock  
NEWS 3 JUL 20 Powerful new interactive analysis and visualization software,  
STN AnaVist, now available  
NEWS 4 AUG 11 STN AnaVist workshops to be held in North America  
NEWS 5 AUG 30 CA/CAPLUS -Increased access to 19th century research documents  
NEWS 6 AUG 30 CASREACT - Enhanced with displayable reaction conditions  
NEWS 7 SEP 09 ACD predicted properties enhanced in REGISTRY/ZREGISTRY  
NEWS 8 OCT 03 MATHDI removed from STN  
NEWS 9 OCT 04 CA/CAPLUS-Canadian Intellectual Property Office (CIPO) added  
to core patent offices  
NEWS 10 OCT 06 STN AnaVist workshops to be held in North America  
NEWS 11 OCT 13 New CAS Information Use Policies Effective October 17, 2005  
NEWS 12 OCT 17 STN(R) AnaVist(TM), Version 1.01, allows the export/download  
of CAPLUS documents for use in third-party analysis and  
visualization tools

NEWS EXPRESS JUNE 13 CURRENT WINDOWS VERSION IS V8.0, CURRENT  
MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),  
AND CURRENT DISCOVER FILE IS DATED 13 JUNE 2005

NEWS HOURS STN Operating Hours Plus Help Desk Availability  
NEWS INTER General Internet Information  
NEWS LOGIN Welcome Banner and News Items  
NEWS PHONE Direct Dial and Telecommunication Network Access to STN  
NEWS WWW CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that  
specific topic.

All use of STN is subject to the provisions of the STN Customer  
agreement. Please note that this agreement limits use to scientific  
research. Use for software development or design or implementation  
of commercial gateways or other similar uses is prohibited and may  
result in loss of user privileges and other penalties.

\* \* \* \* \* STN Columbus \* \* \* \* \*

FILE 'HOME' ENTERED AT 18:20:23 ON 17 OCT 2005

=> file agricola biosis caplus  
COST IN U.S. DOLLARS

FULL ESTIMATED COST

SINCE FILE	TOTAL
ENTRY	SESSION
0.21	0.21

FILE 'AGRICOLA' ENTERED AT 18:20:46 ON 17 OCT 2005

FILE 'BIOSIS' ENTERED AT 18:20:46 ON 17 OCT 2005  
Copyright (c) 2005 The Thomson Corporation

FILE 'CAPLUS' ENTERED AT 18:20:46 ON 17 OCT 2005  
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.  
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

=> s lipase

L1 85115 LIPASE

=> l1 and senescence

L1 IS NOT A RECOGNIZED COMMAND

The previous command name entered was not recognized by the system.  
For a list of commands available to you in the current file, enter  
"HELP COMMANDS" at an arrow prompt (=>).

=> s l1 and senescence

L2 190 L1 AND SENESCENCE

=> s l2 and (transgenic or transform?)

L3 14 L2 AND (TRANSGENIC OR TRANSFORM?)

=> d his

(FILE 'HOME' ENTERED AT 18:20:23 ON 17 OCT 2005)

FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 18:20:46 ON 17 OCT 2005

L1 85115 S LIPASE

L2 190 S L1 AND SENESCENCE

L3 14 S L2 AND (TRANSGENIC OR TRANSFORM?)

=> d ti

L3 ANSWER 1 OF 14 AGRICOLA Compiled and distributed by the National  
Agricultural Library of the Department of Agriculture of the United States  
of America. It contains copyrighted materials. All rights reserved.  
(2005) on STN

TI Altered membrane **lipase** expression delays leaf  
**senescence**.

=> dup rem l3

PROCESSING COMPLETED FOR L3

L4 12 DUP REM L3 (2 DUPLICATES REMOVED)

=> d ab l4

L4 ANSWER 1 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN

AB Identification of blood-based biomarkers with predictive power in  
directing clin. outcomes is an active area of clin. research. Methods are  
provided for determining whether a subject has a graft tolerant phenotype.  
Global gene expression monitoring is used to test whether blood-based  
markers for diagnostic of spontaneously achieved tolerance could be  
identified in a cohort of long-term renal transplant patients. By  
normalizing to the average expression levels in normal control blood samples,  
several functional groups of genes were identified to be at significantly  
higher levels in the tolerant patients, where the identified genes  
included genes characteristic of rapid cell proliferation, anti-apoptotic  
activity and **senescence**, as well as genes involved in immune  
signaling cascades including specific transcription factors, cell adhesion  
mols. Overall the data shows that the spontaneously achieved state of  
immunotolerance is an active regulatory process as evidenced by the large  
nos. of up-regulated genes relative to normal blood and by the highly  
synchronized expression signature that is observed. The methods and compns.  
find use in a variety of applications, including the determination of an  
immunosuppressive therapy regimen.

=> d l4 ab 1-12

L4 ANSWER 1 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN

AB Identification of blood-based biomarkers with predictive power in  
directing clin. outcomes is an active area of clin. research. Methods are  
provided for determining whether a subject has a graft tolerant phenotype.

- Global gene expression monitoring is used to test whether blood-based markers for diagnostic of spontaneously achieved tolerance could be identified in a cohort of long-term renal transplant patients. By normalizing to the average expression levels in normal control blood samples, several functional groups of genes were identified to be at significantly higher levels in the tolerant patients, where the identified genes included genes characteristic of rapid cell proliferation, anti-apoptotic activity and **senescence**, as well as genes involved in immune signaling cascades including specific transcription factors, cell adhesion molecules. Overall the data shows that the spontaneously achieved state of immunotolerance is an active regulatory process as evidenced by the large numbers of up-regulated genes relative to normal blood and by the highly synchronized expression signature that is observed. The methods and compounds find use in a variety of applications, including the determination of an immunosuppressive therapy regimen.

L4 ANSWER 2 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN

AB The present invention provides methods for diagnosing mental disorders (e.g., psychotic disorders such as schizophrenia). The present invention uses DNA microarray analysis to demonstrate differential expression of genes in selected regions of post-mortem brains from patients diagnosed with mental disorders in comparison with normal control subjects. The invention also provides methods of identifying modulators of such mental disorders as well as methods of using these modulators to treat patients suffering from such mental disorders.

L4 ANSWER 3 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN

AB Regulation of expression of **senescence** in plants is achieved by integration of a gene or gene fragment encoding **senescence**-induced **lipase** into the plant genome in antisense orientation. The carnation and Arabidopsis genes encoding **senescence**-induced **lipase** are identified and the nucleotide sequences are used to modify **senescence** in **transgenic** plants.

L4 ANSWER 4 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN

AB This invention provides reagents and methods for identifying genes whose expression is modulated by induction of CDK inhibitor gene expression. The invention also provides reagents and methods for identifying compounds that inhibit the effects of CDK inhibitors such as p21, p27 and p16 on cellular gene expression, as a first step in rational drug design for preventing pathogenic consequences of cellular **senescence**, such as carcinogenesis and age-related diseases.

L4 ANSWER 5 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN

AB Regulation of expression of **senescence** in plants is achieved by integration of a gene or gene fragment encoding **senescence**-induced **lipase** into the plant genome in antisense orientation. This results in inhibition of **senescence**-induced **lipase** gene which increases resistance of plants to environmental stress-induced **senescence**, enhanced biomass of the plant and increased seed yield. This method has been applied to fruit-bearing plants, flowering plants, vegetables, agronomic crop plants and forest species. The carnation and Arabidopsis genes encoding **senescence**-induced **lipase** are identified and the nucleotide sequences are used to modify **senescence** in **transgenic** plants.

L4 ANSWER 6 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN

AB The invention discloses methods, gene databases, gene arrays, protein arrays, and devices that may be used to determine the hypersensitivity of individuals to a given agent, such as drug or other chemical, in order to prevent toxic side effects. In one embodiment, methods of identifying hypersensitivity in a subject by obtaining a gene expression profile of multiple genes associated with hypersensitivity of the subject suspected to be hypersensitive, and identifying in the gene expression profile of the subject a pattern of gene expression of the genes associated with hypersensitivity are disclosed. The gene expression profile of the subject may be compared with the gene expression profile of a normal individual and a hypersensitive individual. The gene expression profile of the subject that is obtained may comprise a profile of levels of mRNA

- or cDNA. The gene expression profile may be obtained by using an array of nucleic acid probes for the plurality of genes associated with hypersensitivity. The expression of the genes predetd. to be associated with hypersensitivity is directly related to prevention or repair of toxic damage at the tissue, organ or system level. Gene databases arrays and apparatus useful for identifying hypersensitivity in a subject are also disclosed.

L4 ANSWER 7 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN

AB Chlorophyllase from *Chenopodium album* and *Arabidopsis thaliana*, and cDNAs, and **transgenic** plants **transformed** with them, are disclosed. Chlorophyllase (Chlase) is the first enzyme involved in chlorophyll (Chl) degradation and catalyzes the hydrolysis of ester bond to yield chlorophyllide and phytol. In the present study, we isolated the Chlase cDNA. We synthesized degenerate oligo DNA probes based on the internal amino acid sequences of purified Chlase from *Chenopodium album*, screened the *C. album* cDNA library, and cloned a cDNA (CaCLH, *C. album* chlorophyll-chlorophyllido hydrolase). The deduced amino acid sequence (347 aa residues) had a **lipase** motif overlapping with an ATP/GTP-binding motif (P-loop). CaCLH possibly was localized in the extraplastidic part of the cell, because a putative signal sequence for endoplasmic reticulum is at the N terminus. The amino acid sequence shared 37% identity with a function-unknown gene whose mRNA is inducible by coronatine and methyljasmonate (MeJA) in *Arabidopsis thaliana* (AtCLH1). We expressed the gene products of AtCLH1 and of CaCLH in *Escherichia coli*, and they similarly exhibited Chlase activity. Moreover, we isolated another full-length cDNA based on an *Arabidopsis* genomic fragment and expressed it in *E. coli*, demonstrating the presence of the second *Arabidopsis* CLH gene (AtCLH2). No typical feature of signal sequence was identified in AtCLH1, whereas AtCLH2 had a typical signal sequence for chloroplast. AtCLH1 mRNA was induced rapidly by a treatment of MeJA, which is known to promote **senescence** and Chl degradation in plants, and a high mRNA level was maintained up to 9 h. AtCLH2, however, did not respond to MeJA.

L4 ANSWER 8 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN

AB Regulation of expression of **senescence** in plants is achieved by integration of a gene or gene fragment encoding **senescence**-induced **lipase** into the plant genome in antisense orientation. The carnation gene encoding **senescence**-induced **lipase** is identified and the nucleotide sequence is used to modify **senescence** in **transgenic** plants.

L4 ANSWER 9 OF 12 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2005) on STN .DUPLICATE 1

L4 ANSWER 10 OF 12 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

AB When studying the **senescence** of lupine, soybean and bean nodules, special attention was paid to structural and functional organization of the nitrogen-fixing symbiotic system and specifics of pro- and eukaryotic cell relationships. It was shown that changes in the ultrastructure of macrosymbiont (a decrease in ribosome number, vesiculation of granular endoplasmic reticulum and Golgi apparatus dictyosomes, mitochondrial swelling, and nucleoplasmic clarification) and microsymbiont (increased peribacteroid space (PBS) volume, symbiosome fusion, bacteroid lysis) took place during aging. Experiments proved that during **senescence**, PBS became a lytic compartment exhibiting acid phosphatase and **lipase** activities. The enzymes entered PBS by fusion of primary lysosomes with peribacteroid membrane. At the same time, symbiosome **transformed** into secondary lysosome where bacteroid lysis took place. During effective symbiosis, nodule **senescence** in many legumes took place at the end of the reproductive phase. In noneffective nodules (plant infection with *Rhizobium*), bacteria did not **transform** into bacteroids and quickly aged in the infected cells. Abnormal symbiosome structure was observed during this process as was degradation of plant cell immature

- bacteroids and organelles. Drought, hypoxia, darkness and high calcium doses accelerated nodule **senescence**. *Rhizobium leguminosarum* and *Bradyrhizobium lupini* were used for seed inoculation.

L4 ANSWER 11 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN

AB **Senescence** of lupine, soybean, and broad bean nodules was studied with emphasis on the structural and functional organization of the symbiotic tissue and specific interrelations between pro- and eukaryotic cells. Some **senescence**-related changes were observed in the ultrastructure of both macrosymbiont (a decrease in the number of ribosomes, vesicle formation from granular endoplasmic reticulum and Golgi dictyosomes, mitochondria swelling, and nucleoplasm lightening) and microsymbiont (an increase in the volume of the peribacteroid space (PBS), a symbiosome fusion, and a lysis of bacteroids). The PBS was exptl. shown to become a lytic compartment during nodule **senescence**, with the activities of acid phosphatase and **lipase** within it. These enzymes entered into the PBS from primary lysosomes after peribacteroid and lysosome membranes were fused. As a result, symbiosomes were **transformed** into secondary lysosomes exerting a bacteroid lysis. Nodule **senescence** in many legumes inoculated with effective rhizobium strains commenced by the end of the reproductive phase. In ineffective nodules (inoculation with fix- rhizobia), bacteria in infected cells failed to **transform** into bacteroids and senesced very rapidly. In this case, symbiosomes had an anomalous structure, and undeveloped bacteroids and plant cell organelles degraded. Some unfavorable environmental factors (drought, hypoxia, darkness, calcium excess) accelerated nodule **senescence**.

L4 ANSWER 12 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN

AB Aged mice exhibit an increase in their body weight (BW), which is associated with fat deposit increase. Epidermal growth factor (EGF) concentration in the submandibular gland also increases with aging. The authors examined the effects of elevated EGF on the adiposity of aged female mice. Studies were started in two groups of animals consisting of sham-operated and sialoadenectomized (Sx; surgical removal of the submandibular glands) mice at 8 wk of age. Body weight gain and food intake were measured throughout 78 wk of age in these two groups. Body weight was significantly less in the Sx group throughout 78 wk, while food intake was not changed by Sx after 12 wk of age. To examine further if EGF plays a role in the induction of adiposity in aged female mice, sham-operated animals were given 100 µl anti-EGF rabbit antiserum (anti-EGF group) or normal rabbit serum (control group) every 3 days, and Sx animals were given 5 µg/day EGF (Sx + EGF group) or saline (Sx group) from 78 wk of age for 3 wk. At 81 wk of age, all animals of these four groups were killed, and carcass fat deposition and fat cell sizes were measured. Although the relative wts. (weight ratio to BW) of the liver and kidney were not changed by Sx and anti-EGF treatment, the relative wts. of mesenteric and s.c. fat tissues and adipocyte wts. were significantly decreased in Sx and anti-EGF groups compared with the control group. Moreover, both acyl-CoA synthetase (ACS) and lipoprotein **lipase** (LPL) mRNA levels were significantly decreased by Sx or anti-EGF administration in mesenteric and s.c. fat tissues. EGF administration to Sx animals had no effect on BW, fat tissues and adipocyte wts., and ACS and LPL mRNA levels. The results, however, were consistent with the fact that adipose tissue EGF receptors were down regulated in Sx mice. These findings suggest that EGF may play a role in the induction of adiposity in aged female mice.